

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 17, 2005, 23:58:38 ; Search time 42 Seconds
(without alignments)
579.419 Million cell updates/sec

Title: SEQ2-129X-307X
Perfect score: 1743

Sequence: 1 ASTKGPSVPLAPCSRSTSE.....XHEALHNHYTQKSLSLSPSK 326

Scoring table: BLOSUM62DX
Gapopen 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649054 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing First 45 summaries

Database : Issued_Patents_AA:*

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5: /cgn2_6/ptodata/1/iaa/PCRTUS_COMBO.pep:
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1743	100.0	326	2	US-0-8-656-586-9	Sequence 9, Appli
2	1731	99.3	451	4	US-0-9-472-087-70	Sequence 70, Appli
3	1731	99.3	463	4	US-0-9-472-087-71	Sequence 1, Appli
4	1731	99.3	463	4	US-0-9-472-087-74	Sequence 63, Appli
5	1731	99.3	463	4	US-0-9-472-087-63	Sequence 68, Appli
6	1731	99.3	463	4	US-0-9-472-087-68	Sequence 2, Appli
7	1731	99.3	464	4	US-0-9-472-087-72	Sequence 66, Appli
8	1731	99.3	464	4	US-0-9-472-087-66	Sequence 28, Appli
9	1731	99.3	470	4	US-0-9-859-053-28	Sequence 32, Appli
10	1731	99.3	470	4	US-0-9-859-053-32	Sequence 36, Appli
11	1731	99.3	470	4	US-0-9-859-053-36	Sequence 4, Appli
12	1731	99.3	530	3	US-0-9-477-460B-4	Sequence 4, Appli
13	1731	99.3	530	3	US-0-8-319-516-4	Sequence 4, Appli
14	1731	99.3	530	3	US-0-9-329-916-4	Sequence 4, Appli
15	1731	99.3	530	3	US-0-8-485-372A-4	Sequence 4, Appli
16	1731	99.3	530	4	US-0-9-409-006A-4	Sequence 4, Appli
17	1731	99.3	530	4	US-0-8-484-681-4	Sequence 4, Appli
18	1731	99.3	530	4	US-0-9-766-995-4	Sequence 4, Appli
19	1731	99.3	530	5	PCT-US93-07422-4	Sequence 4, Appli
20	1728.5	99.2	462	4	US-0-9-627-896B-24	Sequence 24, Appli
21	1725	99.0	463	4	US-0-9-472-087-64	Sequence 64, Appli
22	1720	98.7	450	2	US-0-8-788-800-12	Sequence 12, Appli
23	1720	98.7	469	2	US-0-9-914-373C-23	Sequence 23, Appli
24	1720	98.7	469	3	US-0-8-417-642B-23	Sequence 23, Appli
25	1720	98.7	469	4	US-0-9-206C-23	Sequence 23, Appli
26	1720	98.7	469	4	US-0-9-686C-23	Sequence 23, Appli
27	1720	98.7	469	4	US-0-9-705-392A-23	Sequence 23, Appli

RESULT 1
US-08-656-586-9

/ Sequence 9, Application US/08655586

/ Patent No. 5834597

/ GENERAL INFORMATION:

APPLICANT: Tso, J. Yun

APPLICANT: Cole, Michael S.

APPLICANT: Arasetti, Claudio

TITLE OF INVENTION: Mutated No. 5834597activating IgG2 Domains and

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/656-586

FILING DATE: 31-MAY-1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Liebeschuetz, Joseph O.

REGISTRATION NUMBER: 17,505

REFERENCE/DOCKET NUMBER: 11823-007210US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 326 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE: Protein

NAME/KEY: Protein

LOCATION: 1. 326

OTHER INFORMATION: /note= "heavy chain constant region of

IgG2 mutant 3"

US-08-656-586-9

Query Match Similarity 100.0%; Score 1743; DB 2; Length 326;

Best Local Similarity .99.4%; Pred. No. 3.4e-153;

Matches 324; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 ASTKGPSVFLAPCPSRSTSESTAALGCLVKDVKYFPEPVTVSNNSGALTSGVHTFPAVLOSS 60
 1 ASTKGPSVFLAPCPSRSTSESTAALGCLVKDVKYFPEPVTVSNNSGALTSGVHTFPAVLOSS 60

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 61 GLYSLSSSVVTPSSNFGTQTYTCNDHKPSNTKVDKTVVERKCCVECPCPAPAAAPSVF 120

121 LFPPKPKDXLMIISRTPBVTCTVVDYSHEDPVOFNMVYDGVEVHNNAKTKPREEQFNSTFR 180
 121 LFPPKPKDXLMIISRTPBVTCTVVDYSHEDPVOFNMVYDGVEVHNNAKTKPREEQFNSTFR 180

181 VVSLLTVVHQWLNGKEYKCKVSNKGLPAPLEKTISKTKGGPREPOVYTLPPSREEMTKN 240
 181 VVSLLTVVHQWLNGKEYKCKVSNKGLPAPLEKTISKTKGGPREPOVYTLPPSREEMTKN 240

241 QVSLLTCLVKGYPSDIAVEWESNGQPENNYKTPPMQLDSDSFFLYSKLTVDKSRWQGN 300
 241 QVSLLTCLVKGYPSDIAVEWESNGQPENNYKTPPMQLDSDSFFLYSKLTVDKSRWQGN 300

301 VFSCSVXHEALTHNNHYTOKSLSLSPSK 326
 301 VFSCSVXHEALTHNNHYTOKSLSLSPSK 326

SUMT 2
 US-09-472-087-0
 Sequence 70, Application US/09472087
 Patent No. 6682736

GENERAL INFORMATION:
 APPLICANT: HANSON, DOUGLAS C.
 APPLICANT: NEVEU, MARK J.
 APPLICANT: MUELLER, EILLEN E.
 APPLICANT: HANKE, JEFFREY H.
 APPLICANT: GILMAN, STEVEN C.
 APPLICANT: DAVIS, C. GEOFFREY
 APPLICANT: CORVALAN, JOSE R.
 TITLE OF INVENTION: HUMAN MONOClonAL ANTIBODIES TO CTLA-4
 FILE REFERENCE: ABX-PFI
 CURRENT APPLICATION NUMBER: US/09/472 087
 CURRENT FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: 60/113.647
 PRIOR FILING DATE: 1998-12-23
 NUMBER OF SEQ ID NOS: 147
 SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1
 LENGTH: 463
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-472-087-1

Query Match 99.3%; Score 1731; DB 4; Length 463;
 Best Local Similarity 98.5%; Pred. No. 7.1e-152;
 Matches 321; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 ASTKGPSVFLAPCPSRSTSESTAALGCLVKDVKYFPEPVTVSNNSGALTSGVHTFPAVLOSS 60
 1 ASTKGPSVFLAPCPSRSTSESTAALGCLVKDVKYFPEPVTVSNNSGALTSGVHTFPAVLOSS 60

126 ASTKGPSVFLAPCPSRSTSESTAALGCLVKDVKYFPEPVTVSNNSGALTSGVHTFPAVLOSS 185
 126 ASTKGPSVFLAPCPSRSTSESTAALGCLVKDVKYFPEPVTVSNNSGALTSGVHTFPAVLOSS 185

61 GLYSLSSSVVTPSSNFGTQTYTCNDHKPSNTKVDKTVVERKCCVECPCPAPAAAPSVF 120
 61 GLYSLSSSVVTPSSNFGTQTYTCNDHKPSNTKVDKTVVERKCCVECPCPAPAAAPSVF 120

186 GLYSLSSSVVTPSSNFGTQTYTCNDHKPSNTKVDKTVVERKCCVECPCPAPVGPSVF 245
 186 GLYSLSSSVVTPSSNFGTQTYTCNDHKPSNTKVDKTVVERKCCVECPCPAPVGPSVF 245

RESULT 3
 US-09-472-087-1
 Sequence 1, Application US/09472087
 Patent No. 6682736

GENERAL INFORMATION:
 APPLICANT: HANSON, DOUGLAS C.
 APPLICANT: NEVEU, MARK J.
 APPLICANT: MUELLER, EILLEN E.
 APPLICANT: HANKE, JEFFREY H.
 APPLICANT: GILMAN, STEVEN C.
 APPLICANT: DAVIS, C. GEOFFREY
 APPLICANT: CORVALAN, JOSE R.
 TITLE OF INVENTION: HUMAN MONOClonAL ANTIBODIES TO CTLA-4
 FILE REFERENCE: ABX-PFI
 CURRENT APPLICATION NUMBER: US/09/472 087
 CURRENT FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: 60/113.647
 PRIOR FILING DATE: 1998-12-23
 NUMBER OF SEQ ID NOS: 147
 SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1
 LENGTH: 463
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-472-087-1

Query Match 99.3%; Score 1731; DB 4; Length 463;
 Best Local Similarity 98.5%; Pred. No. 7.4e-152;
 Matches 321; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 ASTKGPSVFLAPCPSRSTSESTAALGCLVKDVKYFPEPVTVSNNSGALTSGVHTFPAVLOSS 60
 1 ASTKGPSVFLAPCPSRSTSESTAALGCLVKDVKYFPEPVTVSNNSGALTSGVHTFPAVLOSS 60

61 GLYSLSSSVVTPSSNFGTQTYTCNDHKPSNTKVDKTVVERKCCVECPCPAPAAAPSVF 120
 61 GLYSLSSSVVTPSSNFGTQTYTCNDHKPSNTKVDKTVVERKCCVECPCPAPAAAPSVF 120

126 ASTKGPSVFLAPCPSRSTSESTAALGCLVKDVKYFPEPVTVSNNSGALTSGVHTFPAVLOSS 305
 126 ASTKGPSVFLAPCPSRSTSESTAALGCLVKDVKYFPEPVTVSNNSGALTSGVHTFPAVLOSS 305

301 VFSCSVXHEALTHNNHYTOKSLSLSPSK 326
 301 VFSCSVXHEALTHNNHYTOKSLSLSPSK 326

438 VFSCSVXHEALTHNNHYTOKSLSLSPSK 463
 438 VFSCSVXHEALTHNNHYTOKSLSLSPSK 463

RESULT 4
 US-09-472-087-4
 Sequence 4, Application US/09472087
 Patent No. 6682736

GENERAL INFORMATION:
 APPLICANT: HANSON, DOUGLAS C.
 APPLICANT: NEVEU, MARK J.
 APPLICANT: MUELLER, EILLEN E.
 APPLICANT: HANKE, JEFFREY H.
 APPLICANT: GILMAN, STEVEN C.
 APPLICANT: DAVIS, C. GEOFFREY
 APPLICANT: CORVALAN, JOSE R.

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protein - protein search, using sw model

on: November 17, 2005, 23:47:57 ; Search time 164 Seconds
(without alignments)
tie: SE02-129X-307X
effect score: 1743
quence: 1 ASTKGPSVPELAPCSRSTSE.....xHEALHNHTQKSLSLSPSK 326

oring table: BlOsum62DX
Gapext 0.5

arched: 2105692 seqs, 386760381 residues

tal number of hits satisfying chosen parameters: 2105692

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqp1980s;*
2: Geneseqp1990s;*
3: Geneseqp2000s;*
4: Geneseqp2001s;*
5: Geneseqp2002s;*
6: Geneseqp2003as;*
7: Geneseqp2003bs;*
8: Geneseqp2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

built	No.	Query	Score	Match	Length	DB	ID	Description
1	1743	100.0	326	8	ADN33229			Adn33229 IgGm3-CH
2	1738	99.7	326	2	AAW36163			Aaw36163 Heavy chain
3	1731	99.3	326	4	AAB02643			Aae02643 Human imm
4	1731	99.3	326	5	AA47857			Aam47857 Human Ig-
5	1731	99.3	326	5	ABG30462			Abg30462 Human ant
6	1731	99.3	326	5	ABG77148			Abg77148 Anti-IGF-
7	1731	99.3	326	6	AAB32916			Aae32916 Human imm
8	1731	99.3	326	6	AAB32628			Aae32628 Human imm
9	1731	99.3	326	6	AAB30894			Aac30894 Human imm
10	1731	99.3	326	7	ADB97353			Ad97353 Human IgG
11	1731	99.3	326	7	ADF75002			Adf75002 Human Ig
12	1731	99.3	326	8	ADM41541			Adm41541 Anti-inte
13	1731	99.3	326	8	ADG95469			Adg95469 Human IgG
14	1731	99.3	326	8	ADR28562			Adr28562 Human ant
15	1731	99.3	445	2	AY31670			Aay31670 Human IgG
16	1731	99.3	445	8	ADK52332			Adk52332 Human ant
17	1731	99.3	445	8	ADK52384			Adk52384 Human ant
18	1731	99.3	445	8	ADK52296			Adk52296 Human ant
19	1731	99.3	445	8	ADK52312			Adk52312 Human ant
20	1731	99.3	451	3	AAV93734			Aay93734 The heavy
21	1731	99.3	451	6	AAE35889			Aae35889 Human IgG
22	1731	99.3	458	8	ADP07903			Adp07903 Human imm
23	1731	99.3	462	3	AAB26884			Aab26884 Human imm
24	1731	99.3	463	3	AAV93701			Aay93701 The heavy
25	1731	99.3	463	3	AAV93727			Aay93727 The heavy

RESULT 1
ID: ADN33229 standard; protein: 326 AA.
XX ADN33229;
AC AC
XX XX 18-NOV-2004 (First entry)
DT DT
XX DE IgGm3-CH heavy chain constant region.
XX KW IgGm3-CH; antibody; IgG; heavy chain constant region;
KW FcRn binding; affinity; asthma; autoimmune disease; cancer;
KW viral infection; antiasthmatic; immunosuppressive; cytostatic; virucide.
XX OS Unidentified.
XX PN WO2004035752-A2.
XX PD 29-APR-2004.
XX PP 15-OCT-2003; 2003WO-US033037.
XX PR 15-OCT-2002; 2002US-0418972P.
PR 10-APR-2003; 2003US-0462014P.
PR 03-JUN-2003; 2003US-0495762P.
PR 29-AUG-2003; 2003US-0499048P.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PI Hinton PR, Tsurushita N, Tso YJ, Vasquez M,
XX DR Disclosure: SEQ ID NO 2; 140PP; English.
XX PT New modified antibody of class IgG having an altered FcRn binding
affinity and/or serum half-life, useful in immunology and protein
engineering, and for diagnosing or treating asthma, autoimmune diseases,
cancer and viral infections.
XX PS Disclosure: SEQ ID NO 2; 140PP; English.

The invention relates to a modified antibody of class IgG where at least one amino acid residue in the heavy chain constant region is different from that present in an unmodified class IgG antibody, and where the FcRn binding affinity and/or serum half-life of the modified antibody is altered relative to that of the unmodified antibody. The methods and compositions of the present invention are useful in the fields of immunology and protein engineering, in particular for using modified class IgG antibodies for diagnosing and treating asthma, autoimmune

diseases, cancer and viral infections. This sequence represents the antibody IgGm3-CH heavy chain constant region of the invention.

Sequence 326 AA:

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Query Match      100.0%; Score 1743; DB 8; Length 326;
Best Local Similarity 99.4%; Pred. No. 4.2e-126;
Matches 324; Conservative 2; Mismatches 0; Gaps 0;

1 ASTKCPSPVPLAPCSRSTESTAALGLCKVYKDFFPEPVTVSNNSGALTSGVHTPVALQSS 60
1 ASTKCPSPVPLAPCSRSTESTAALGLCKVYKDFFPEPVTVSNNSGALTSGVHTPVALQSS 60
61 GLYSISSVVTPPSSNFGTQTYTCVNDHKPSNTVKDVTVERKCCVCPCPAPPAAAPSVF 120
61 GLYSISSVVTPPSSNFGTQTYTCVNDHKPSNTVKDVTVERKCCVCPCPAPPAAASVF 120
121 LFPPPKPDKXLMISRTPDPEVOTWYDGVVEVHNAKTKPREEQFNSTFR 180
121 LFPPPKPDKXLMISRTPDPEVOTWYDGVVEVHNAKTKPREEQFNSTFR 180
181 VVSILTVVHQDWLNGKEYKCKVSNKGGLPAPIETKISKTKGQPPEPVTVLPSREENTKN 240
181 VVSILTVVHQDWLNGKEYKCKVSNKGGLPAPIETKISKTKGQPPEPVTVLPSREENTKN 240
241 QVSLLTCLVKGFYPSPDIAWEWSNQEPENNYKTPMLSDGSFLYSLKLTVDKSRWQGN 300
241 QVSLLTCLVKGFYPSPDIAWEWSNQEPENNYKTPMLSDGSFLYSLKLTVDKSRWQGN 300
301 VFSCSVXHEALHNHYTOKSLSLSPSK 326
301 VFSCSVXHEALHNHYTOKSLSLSPSK 326
301 VFSCSVXHEALHNHYTOKSLSLSPSK 326

```

SULT 2
AAW36163 standard; protein; 326 AA.

AAW36163;

22-MAY-1998 (first entry)

Heavy chain constant region of IgG2 mutant 3.

Mutant; immunoglobulin G2; IgG2; heavy chain; constant region; low mitogenic response; human T-cell; immunosuppressant; diagnosis; immune system disease.

Homo sapiens.
Synthetic.

WO9744362-A1.

27-NOV-1997.

19-MAY-1997; 97WO-US008576.

20-MAY-1996; 96US-00650410.
31-MAY-1996; 96US-00656586.

(PROT-) PROTEIN DESIGN LABS INC.
(HUTC-) HUTCHINSON CANCER RES CENT FRED.

Tso JY, Cole MS, Anasetti C;

WPI; 1998-018436/02.

Mutated immunoglobulin G2 constant region that does not induce T cell proliferation - and anti-CD3 antibodies containing this region for use as immunosuppressant with reduced side effects.

Claim 6; Fig 4; 63pp; English.

The present sequence was used in the development of a novel mutated immunoglobulin G (IgG) 2 constant region (CR), having a non-natural segment of amino acids between 234 and 237 (EU numbering system), so that an antibody (Ab) containing the variable region of an anti-CD3 Ab linked to the CR induces lower mitogenic response in human T-cells than does a similar Ab containing the natural IgG2 constant region. The Ab are useful as immunosuppressant, e.g. in autoimmune disease (including rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease), transplant rejection, graft versus host disease, inflammation allergy or sepsis, particularly acute episodes of autoimmune diseases. The Ab can also be used for diagnosis of immune system disease and for determining T cell numbers in patients with acquired immune deficiency syndrome (AIDS). The Ab have fewer side effects than known anti-CD3 Ab, as they do not, in most patients, induce mitogenesis through specific binding to Fc gamma receptors, nor release of cytokines. Compared with F(ab')2 fragments, the Ab have a longer half-life

xx

Sequence 326 AA;

Query Match	99.7%;	Score 1738;	DB 2;	Length 326;
Best Local Similarity	99.1%;	Pred. No. 1e-125;		
Matches	323;	Mismatches	3;	Gaps 0;
Qy	1 ASTKGPSVFPPLAPCSRSTESTAALGLCKVYKDFFPEPVTVSNNSGALTSGVHTPVALQSS 60	Db	1 ASTKGPSVFPPLAPCSRSTESTAALGLCKVYKDFFPEPVTVSNNSGALTSGVHTPVALQSS 60	
Qy	61 GLYSISSVVTPPSSNFGTQTYTCVNDHKPSNTVKDVTVERKCCVCPCPAPPAAAPSVF 120	Db	61 GLYSISSVVTPPSSNFGTQTYTCVNDHKPSNTVKDVTVERKCCVCPCPAPPAAAPSVF 120	
Qy	121 LFPPPKPDKXLMISRTPDPEVOTWYDGVVEVHNAKTKPREEQFNSTFR 180	Db	121 LFPPPKPDKXLMISRTPDPEVOTWYDGVVEVHNAKTKPREEQFNSTFR 180	
Qy	181 VVSILTVVHQDWLNGKEYKCKVSNKGGLPAPIETKISKTKGQPPEPVTVLPSREENTKN 240	Db	181 VVSILTVVHQDWLNGKEYKCKVSNKGGLPAPIETKISKTKGQPPEPVTVLPSREENTKN 240	
Qy	241 QVSLLTCLVKGFYPSPDIAWEWSNQEPENNYKTPMLSDGSFLYSLKLTVDKSRWQGN 300	Db	241 QVSLLTCLVKGFYPSPDIAWEWSNQEPENNYKTPMLSDGSFLYSLKLTVDKSRWQGN 300	
Qy	301 VFSCSVXHEALHNHYTOKSLSLSPSK 326	Db	301 VFSCSVXHEALHNHYTOKSLSLSPSK 326	
Qy	301 VFSCSVXHEALHNHYTOKSLSLSPSK 326	Db	301 VFSCSVXHEALHNHYTOKSLSLSPSK 326	

RESULT 3

AAE02643 standard; protein; 326 AA.

XX AAE02643;

XX DT 06-AUG-2001. (first entry)

XX Human immunoglobulin G2 constant region mature protein.
XX DE Human immunoglobulin G2 constant region mature protein.
XX KW Human; erythropoietin; EPO; antianaemic; nephrotrophic; anti-HIV;
KW vaccine; haemostatic; immunoglobulin G2; IGG; EPO deficient disease;
KW anaemia; renal failure; Human Immunodeficiency Virus; HIV;
KW haematopoietic growth factor.

XX OS Homo sapiens.

XX PN WO200136489-A2.

XX PD 25-MAY-2001.

XX PR 03-NOV-2000; 2000WO-EP010843.

XX PR 12-NOV-1999; 99US-0164855P.

GenCore version 5.1.6
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protein - protein search, using sw model

on: November 18, 2005, 00:07:19 ; Search time 164 Seconds
 (without alignments)
 631.716 Million cell updates/sec

le: seq2-129x-307x
 ue: 1 ASTKGPSVFLAPCSRSTSE.....XHEALHNHYTQKSLSLSPSK 326

ring table: BL05UM62DX
 Gapext 0.5

rched: 1867879 seqs, 418409474 residues

a1 number of hits satisfying chosen parameters: 1867879

:t-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

.abase : Published Applications AA:
 1: /cgn2_6/pctodata/1/pubcaa/US07_PUBCOMB.pep:
 2: /cgn2_6/pctodata/1/pubcaa/US06_NEWW_PUB.pep:
 3: /cgn2_6/pctodata/1/pubcaa/US06_PUBCOMB.pep:
 4: /cgn2_6/pctodata/1/pubcaa/US07_NEW_PUB.pep:
 5: /cgn2_6/pctodata/1/pubcaa/PCRTUS_PUBCOMB.pep:
 6: /cgn2_6/pctodata/1/pubcaa/US08_NEW_PUB.pep:
 7: /cgn2_6/pctodata/1/pubcaa/US08_PUBCOMB.pep:
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 18: /cgn2_6/pctodata/1/pubcaa/US10F_PUBCOMB.pep:
 19: /cgn2_6/pctodata/1/pubcaa/US11A_PUBCOMB.pep:
 20: /cgn2_6/pctodata/1/pubcaa/US11B_PUBCOMB.pep:
 21: /cgn2_6/pctodata/1/pubcaa/US11C_PUBCOMB.pep:
 22: /cgn2_6/pctodata/1/pubcaa/US60_PUBCOMB.pep:
 23: /cgn2_6/pctodata/1/pubcaa/US60_PUBCOMB.pep:
 24: /cgn2_6/pctodata/1/pubcaa/US60_PUBCOMB.pep:
 25: /cgn2_6/pctodata/1/pubcaa/US60_PUBCOMB.pep:
 26: /cgn2_6/pctodata/1/pubcaa/US60_PUBCOMB.pep:
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ALIGNMENTS

RESULT 1
 US-10-822-300-2
 ; Sequence 2, Application US/10822300
 ; Publication No. US2005014934A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinton, et al.
 ; TITLE OF INVENTION: ALTERATION OF FCRN BINDING AFFINITIES OR SERUM HALF-LIVES OF
 ; PROTEINS; INVENTION: ANTIBODIES BY MUTAGENESIS
 ; FILE REFERENCE: 05882_0039_CBUS01
 ; CURRENT APPLICATION NUMBER: US/10/822,300
 ; CURRENT FILING DATE: 2004-04-09
 ; NUMBER OF SEQ ID NOS: 146
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO: 2
 ; LENGTH: 326
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-822-300-2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sult No.	Score	Query Length	DB ID	Description
1	1743	100.0	326	Sequence 2, Appli
2	1743	100.0	326	Sequence 10, Appli
3	1743	100.0	326	Sequence 11, Appli
4	1743	100.0	326	Sequence 12, Appli
5	1743	100.0	326	Sequence 13, Appli
6	1743	100.0	326	Sequence 14, Appli
7	1743	100.0	326	Sequence 15, Appli
8	1743	100.0	326	Sequence 16, Appli
9	1743	100.0	326	Sequence 17, Appli
10	1743	100.0	326	Sequence 18, Appli
11	1743	100.0	326	Sequence 19, Appli

Query Match 100.0%; Score 1743; DB 17;

Best Local Similarity 99.4%; Pred. No. 6.7e-127;
 Matches 324; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLAPCSRSTSESTAAAGLKVDKYFPEPVTVNSIGALTSGVHTFPAVLOSS 60
 Db 1 ASTKGPSVFLAPCSRSTSESTAAAGLKVDKYFPEPVTVNSIGALTSGVHTFPAVLOSS 60
 Qy 61 GLYSLSVVTVSSNFGTQTYTCNVDHKPNTKVDTVERCCVEPPCPAPPAASVF 120
 Db 61 GLYSLSVVTVSSNFGTQTYTCNVDHKPNTKVDTVERCCVEPPCPAPPAASVF 120
 Qy 121 LPPPKPKDXLMISRTPEVTVYDVSHEDEPEVQFNYYDGVEVHNNAKTKPRBEQFNSTFR 180
 Db 121 LPPPKPKDXLMISRTPEVTVYDVSHEDEPEVQFNYYDGVEVHNNAKTKPRBEQFNSTFR 180

181 VVSVLTVHQDLNGKEYKCKVSNKGLPAPIEKTIKSKTGQPREPOVYTLPSSREEMTKN 240
 181 VVSVLTVHQDLNGKEYKCKVSNKGLPAPIEKTIKSKTGQPREPOVYTLPSSREEMTKN 240
 241 QVSILTCLVKGFPSPDAVEWSNGOPENNYKTPMILDSDGSFFLYSKLTVDKSRWQGN 300
 241 QVSILTCLVKGFPSPDAVEWSNGOPENNYKTPMILDSDGSFFLYSKLTVDKSRWQGN 300
 301 VFSCSYXHEALTHNHYTKSLSLSPSK 326
 301 VFSCSYXHEALTHNHYTKSLSLSPSK 326

ULT 2
 sequence 10, Application US/10822300
 publication No. US20050014934A1
 GENERAL INFORMATION:
 APPLICANT: Hinton, et al.
 TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
 FILE REFERENCE: 05882_0039_CUSO01
 CURRENT APPLICATION NUMBER: US/10/822,300
 CURRENT FILING DATE: 2004-04-09
 NUMBER OF SEQ ID NOS: 146
 SOFTWARE: Patent in version 3.2
 SEQ ID NO 10
 LENGTH: 326
 TYPE: PRT
 ORGANISM: Homo sapiens
 10-822-300-10

Query Match Score 100.0%; Pred. No. 6.7e-127; Length 326;
 best Local Similarity 99.4%; Mismatches 0; Indels 0; Gaps 0;

1 ASTKGPSVPLAPCSRSSTESTAAAGLCLVKDYFPEPVTVWSNSGALTSGVHTFPAVLOSS 60

1 ASTKGPSVPLAPCSRSSTESTAAAGLCLVKDYFPEPVTVWSNSGALTSGVHTFPAVLOSS 60

61 GLYSLSVVTVPSNFGTQTYTCNDHKPSNTKVDKTVERKCCVECPCPDAPPAPAPSVF 120

61 GLYSLSVVTVPSNFGTQTYTCNDHKPSNTKVDKTVERKCCVECPCPDAPPAPAPSVF 120

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121 LFPPKPKDXLMISRTPEVTCVYDVSHEDPEVQFNVYDGVEVHAKTRKEEQFNSTR 180

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181 VVSVLTVHQDLNGKEYKCKVSNKGLPAPIEKTIKSKTGQPREPOVYTLPSSREEMTKN 240

241 QVSILTCLVKGFPSPDAVEWSNGOPENNYKTPMILDSDGSFFLYSKLTVDKSRWQGN 300

241 QVSILTCLVKGFPSPDAVEWSNGOPENNYKTPMILDSDGSFFLYSKLTVDKSRWQGN 300

301 VFSCSYXHEALTHNHYTKSLSLSPSK 326

301 VFSCSYXHEALTHNHYTKSLSLSPSK 326

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61 GLYSLSVVTVPSNFGTQTYTCNDHKPSNTKVDKTVERKCCVECPCPDAPPAPAPSVF 120

61 GLYSLSVVTVPSNFGTQTYTCNDHKPSNTKVDKTVERKCCVECPCPDAPPAPAPSVF 120

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181 VVSVLTVHQDLNGKEYKCKVSNKGLPAPIEKTIKSKTGQPREPOVYTLPSSREEMTKN 240

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241 QVSILTCLVKGFPSPDAVEWSNGOPENNYKTPMILDSDGSFFLYSKLTVDKSRWQGN 300

241 QVSILTCLVKGFPSPDAVEWSNGOPENNYKTPMILDSDGSFFLYSKLTVDKSRWQGN 300

301 VFSCSYXHEALTHNHYTKSLSLSPSK 326

301 VFSCSYXHEALTHNHYTKSLSLSPSK 326

Query Match Score 100.0%; Pred. No. 6.7e-127; Length 326;
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1 ASTKGPSVPLAPCSRSSTESTAAAGLCLVKDYFPEPVTVWSNSGALTSGVHTFPAVLOSS 60

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181 VVSVLTVHQDLNGKEYKCKVSNKGLPAPIEKTIKSKTGQPREPOVYTLPSSREEMTKN 240

181 VVSVLTVHQDLNGKEYKCKVSNKGLPAPIEKTIKSKTGQPREPOVYTLPSSREEMTKN 240

241 QVSILTCLVKGFPSPDAVEWSNGOPENNYKTPMILDSDGSFFLYSKLTVDKSRWQGN 300

241 QVSILTCLVKGFPSPDAVEWSNGOPENNYKTPMILDSDGSFFLYSKLTVDKSRWQGN 300

301 VFSCSYXHEALTHNHYTKSLSLSPSK 326

301 VFSCSYXHEALTHNHYTKSLSLSPSK 326

Query Match Score 100.0%; Pred. No. 6.7e-127; Length 326;
 best Local Similarity 99.4%; Mismatches 0; Indels 0; Gaps 0;

1 ASTKGPSVPLAPCSRSSTESTAAAGLCLVKDYFPEPVTVWSNSGALTSGVHTFPAVLOSS 60

1 ASTKGPSVPLAPCSRSSTESTAAAGLCLVKDYFPEPVTVWSNSGALTSGVHTFPAVLOSS 60

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61 GLYSLSVVTVPSNFGTQTYTCNDHKPSNTKVDKTVERKCCVECPCPDAPPAPAPSVF 120

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121 LFPPKPKDXLMISRTPEVTCVYDVSHEDPEVQFNVYDGVEVHAKTRKEEQFNSTR 180

181 VVSVLTVHQDLNGKEYKCKVSNKGLPAPIEKTIKSKTGQPREPOVYTLPSSREEMTKN 240

181 VVSVLTVHQDLNGKEYKCKVSNKGLPAPIEKTIKSKTGQPREPOVYTLPSSREEMTKN 240

241 QVSILTCLVKGFPSPDAVEWSNGOPENNYKTPMILDSDGSFFLYSKLTVDKSRWQGN 300

241 QVSILTCLVKGFPSPDAVEWSNGOPENNYKTPMILDSDGSFFLYSKLTVDKSRWQGN 300

301 VFSCSYXHEALTHNHYTKSLSLSPSK 326

301 VFSCSYXHEALTHNHYTKSLSLSPSK 326

Query Match Score 100.0%; Pred. No. 6.7e-127; Length 326;
 best Local Similarity 99.4%; Mismatches 0; Indels 0; Gaps 0;

1 ASTKGPSVPLAPCSRSSTESTAAAGLCLVKDYFPEPVTVWSNSGALTSGVHTFPAVLOSS 60

1 ASTKGPSVPLAPCSRSSTESTAAAGLCLVKDYFPEPVTVWSNSGALTSGVHTFPAVLOSS 60

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61 GLYSLSVVTVPSNFGTQTYTCNDHKPSNTKVDKTVERKCCVECPCPDAPPAPAPSVF 120

121 LFPPKPKDXLMISRTPEVTCVYDVSHEDPEVQFNVYDGVEVHAKTRKEEQFNSTR 180

121 LFPPKPKDXLMISRTPEVTCVYDVSHEDPEVQFNVYDGVEVHAKTRKEEQFNSTR 180

181 VVSVLTVHQDLNGKEYKCKVSNKGLPAPIEKTIKSKTGQPREPOVYTLPSSREEMTKN 240

181 VVSVLTVHQDLNGKEYKCKVSNKGLPAPIEKTIKSKTGQPREPOVYTLPSSREEMTKN 240

mult No.	Score	Query Length	DB	ID	Description
1	1731	99.3	326	1 G2HU	Ig Gamma-2 chain C
2	1583.5	90.8	327	1 G4HU	Ig Gamma-4 chain C
3	1582	90.8	330	1 GHGU	Ig Gamma-1 chain C
4	1558.5	89.4	327	2 A23511	Ig Gamma-3 chain C
5	1549.5	88.9	377	2 A60764	Ig Gamma-3 chain C
6	1254	71.9	328	2 I47159	Ig Gamma-2a chain
7	1248	71.6	328	2 I47160	Ig Gamma-2b chain
8	1222	70.1	328	2 I47161	Ig Gamma-3 chain C
9	1212	69.5	328	2 I47158	Ig Gamma-1 chain C
10	1185.5	68.0	323	1 GHRB	Ig Gamma chain C
11	1178.5	67.6	472	2 S31459	Ig Gamma-1 chain -
12	1164	66.8	326	2 PS0017	Ig Gamma-1 chain C
13	1162.5	66.7	72	2 S22980	Ig heavy chain premonoclonal antibody
14	1116	66.3	444	2 PC436	Ig Gamma-2 chain C
15	1105	66.0	329	1 G2GP	Ig Gamma-1 chain C
16	1140	65.4	324	1 G1MS	Ig Gamma-1 chain C
17	1135	65.1	393	1 G1MSM	Ig Gamma-1 chain C
18	1134.5	65.1	374	2 S69339	Ig Gamma-1 chain C
19	1112.9	64.8	255	4 S31866	Ig heavy chain C r
20	1126.5	64.6	308	2 C30534	Ig Gamma-2a chain
21	1120	64.3	322	2 PS0019	Ig Gamma chain C r
22	1118	64.1	234	2 PT0207	Ig Gamma-2b chain
23	1108.5	63.6	333	2 PS0018	Ig Gamma-2c chain
24	1107.5	63.5	329	2 S00847	Ig Gamma-2 chain C
25	1105	63.1	327	2 S06611	Ig Gamma-3 heavy C
26	1096	62.9	289	1 G3H0W1	Ig Gamma-3 chain C
27	1085	62.2	329	1 G3MSC	Ig Gamma-2a chain
28	1082	62.1	330	1 G2MSA	Ig Gamma-2a chain
29	1082	62.1	469	2 S37483	Ig Gamma-2a chain

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
protein - protein search, using sw model
on: November 17, 2005, 23:56:58 ; Search time 40 Seconds
(without alignments)
784.167 Million cell updates/sec
le: SEQ-2-129X-307X
effect score: 1743
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Gapop 10.0 , Gapext 0.5
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al number of hits satisfying chosen parameters: 283416

RESULT 1

G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A90732; A93132; A0248
R;Ellison, J.; Hood, L.;
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant regions
A;Reference number: A93906; MUID:62197621; PMID:6804948
A;Accession: A31906
A;Molecule type: DNA
A;Residues: 1-226 <PBL>
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; P1
A;Note: Lyb-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, B.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional analysis
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A9809
A;Molecule type: protein
A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193 'D', 195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a human IgG2 heavy chain
A;Reference number: A90732; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A9752
A;Molecule type: protein
A;Residues: 1-24, 'E', 26-57, 'EV', 60-85;132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 15, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin IgG2 heavy chain
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A9132
A;Molecule type: protein
A;Residues: 238-275 <HOP>
R;Hofmann, T.; Parr, D.M.
Submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic acid residue
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:490472
A;Contents: annotation; myeloma protein Sa, disulfide bonds

rangione, B.; Milstein, C.; Pink, J.R.L.
ure 221, 145-148, 1969
title: Structural studies of immunoglobulin G.
erence number: A9315; PMID:5782707
ontents: annotation: Sa; disulfide bonds
eme: GDB:IGH62
ross-references: GDB:119338; OMIM:147110
ap position: 14Q32_33-14Q32_33
complex: An immunoglobulin heterotetramer subunit consists of two identical light (kg) n disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la uperfamily: immunoglobulin C region; immunoglobulin homology
eywords: duplication; glycoprotein; heterotetramer; immunoglobulin
0-85/Domain: immunoglobulin homology <IM1>
33-20/Domain: immunoglobulin homology <IM2>
19306/Domain: immunoglobulin homology <IM3>
4/Disulfide bonds: interchain (to light chain) #status experimental
7-83-140-200-246-304/Disulfide bonds: #status experimental
02-103-106-109/Disulfide bonds: interchain (to heavy chain) #status predicted
76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 1731; DB 1; Length 326;
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atches 321; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 ASTKGGSVPFLAPCSRSSTSEATAALGCLVLDYDFPEPTVSWNSGALTSGVHTPAVLQSS 60
1 ASTKGGSVPFLAPCSRSSTSEATAALGCLVLDYDFPEPTVSWNSGALTSGVHTPAVLQSS 60

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61 GLYSLSVVTVPPSNFEGTQTYTCNDHKPSNTYKVDKTVERKCCVECPCPAPP-AAASV 119

62 FLFPBPKPDKXLMISRTPETVTCVVDVSHEDPENQFNNYVDGVEVHNAKTKPREFQFNSTF 179
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63 GLYSLSVVTVPPSNFQTTTCNVDHKPSNTYKVDKTVERKCCVECPCPAPPAAAPSVF 120
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121 LFPPKPDKXLMISRTPETVTCVVDVSHEDPENQFNNYVDGVEVHNAKTKPREFQFNSTF 180
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181 VVSVLTIVHQDWLNGKEYKCKVSNKLPAPEKTIKSTKQPREQQVTLPPSRREMTK 240
181 VVSVLTIVHQDWLNGKEYKCKVSNKLPAPEKTIKSTKQPREQQVTLPPSRREMTK 240

241 QVSLLTCLVKGFYPSDIAVENEENGOPENNYKTPPMQLSDGSFFLYSLKLTVDKSRWQQGN 300
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301 VFSCSYXHEALTHNHYTQKSLSLSPRK 326
301 VFSCSYXHEALTHNHYTQKSLSLSPRK 326

ULT 2

gamma-4 chain C region - human
pecies: Homo sapiens (man)
ate: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
cession: A90933; A90349; A02150
llison, J.; Buxbaum, J.; Hood, L.
1, 11-18, 1981
itle: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
erence number: A90933; PMID:6299662
cession: A90933

residues: 1-327 <ELL>

ross-references: UNIPROT:P01861
ote: the sequence was determined from the germline gene
ink, J.R.L.; Butterly, S.H.; De Vries, G.M.; Milstein, C.
hem. J. 117, 33-47, 1970
itle: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
erence number: A90249; PMID:7020750; PMID:192699
ecule type: protein
esidues: 1-30; 81-326 <PIN>

genetics:

A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147110
A;Mol position: 14Q32_33-14Q32_33
A;INTRONS: 99/1_111/1; 22/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kg) hair disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la uperfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:10-85/Domain: immunoglobulin homology <IM1>
F:90-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:21-83_141-301/247-305/Disulfide bonds: #status predicted
F:106_109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match Score 1583.5; DB 1; Length 327;
Best Local Similarity 91.1%; Pred. No. 2e-102;
Matches 298; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

Qy 1 ASTKGGSVPFLAPCSRSSTSEATAALGCLVLDYDFPEPTVSWNSGALTSGVHTPAVLQSS 60
Db 1 ASTKGGSVPFLAPCSRSSTSEATAALGCLVLDYDFPEPTVSWNSGALTSGVHTPAVLQSS 60

Qy 61 GLYSLSVVTVPPSNFEGTQTYTCNDHKPSNTYKVDKTVERKCCVECPCPAPP-AAASV 119
Db 61 GLYSLSVVTVPPSNFEGTQTYTCNDHKPSNTYKVDKTVERKCCVECPCPAPP-AAASV 119

Qy 120 FLFPBPKPDKXLMISRTPETVTCVVDVSHEDPENQFNNYVDGVEVHNAKTKPREFQFNSTF 179
Db 121 FLFPBPKPDKXLMISRTPETVTCVVDVSHEDPENQFNNYVDGVEVHNAKTKPREFQFNSTF 180

Qy 180 RVSVLTIVHQDWLNGKEYKCKVSNKLPAPEKTIKSTKQPREQQVTLPPSRREMTK 239
Db 181 RVSVLTIVHQDWLNGKEYKCKVSNKLPAPEKTIKSTKQPREQQVTLPPSRREMTK 240

Qy 240 NOVSLLTCLVKGFYPSDIAVENEENGOPENNYKTPPMQLSDGSFFLYSLKLTVDKSRWQQGN 299
Db 241 NOVSLLTCLVKGFYPSDIAVENEENGOPENNYKTPPMQLSDGSFFLYSLKLTVDKSRWQQGN 300

RESIDUE 3
GHHU
Ig Gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Accession: A93133; S36861; S33887; B90563; A91722; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 407-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82224238; PMID:6287432
A;Accession: A93133
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: UNIPROT:P01857; EMBL:Z17370
A;Note: this sequence has the Glm(1) allotypic marker, 97-LysB, and the Glm(1) markers;
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Yakahashi, N.; Ueda, S.; Obata, M.; Nakao, T.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139

BLOSUM62DX						
Gapop 10.0 , Gapext 0.5						
Searched: 1612378 seqs, 512079187 residues						
at number of hits satisfying chosen parameters:						
Minimum DB seq length: 0						
Minimum DB seq length: 2000000000						
t-processing: Minimum Match 0%						
Maximum Match 100%						
Listing First 45 summaries						
Database :						
UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl: *						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
	Query No.	Score	Match Length	DB ID	Description	
1	1731	99.3	326	1 GC2_HUMAN	P01859 homo sapien	
2	1731	99.3	417	2 Q6N093	Q6N093 homo sapien	
3	1726	99.0	465	2 Q6P6C4	Q6P6C4 homo sapien	
4	1717	98.5	493	2 Q6GCN4	Q6GCN4 homo sapien	
5	1716	98.5	464	2 Q6MZU6	Q6MZU6 homo sapien	
6	1588	91.1	348	2 Q6PYX1	Q6PYX1 homo sapien	
7	1588	91.1	478	2 Q6I181	Q6I181 homo sapien	
8	1588	91.1	480	2 Q6PUF1	Q6PUF1 homo sapien	
9	1583.5	90.8	327	1 GC4_HUMAN	P01861 homo sapien	
10	1583.5	90.8	473	2 Q8TC63	Q8TC63 homo sapien	
11	1582	90.8	330	1 GC1_HUMAN	P01857 homo sapien	
12	1582	90.8	465	2 Q6GMX6	Q6GMX6 homo sapien	
13	1582	90.8	466	2 Q6INT7	Q6INT7 homo sapien	
14	1582	90.8	469	2 Q7Z7PS	Q7Z7PS homo sapien	
15	1582	90.8	470	2 Q6DFA4	Q6DFA4 homo sapien	
16	1582	90.8	473	2 Q7Z5W1	Q7Z5W1 homo sapien	
17	1578	90.5	475	2 Q6N089	Q6N089 homo sapien	
18	1582	90.8	480	2 Q6N094	Q6N094 homo sapien	
19	1582	90.8	476	2 Q6GMW7	Q6GMW7 homo sapien	
20	1510.5	90.7	476	2 Q6HZX7	Q6HZX7 homo sapien	
21	1578	90.5	473	2 Q6MVY7	Q6MVY7 homo sapien	
22	1578	90.5	473	2 Q6P055	Q6P055 homo sapien	
23	1578	90.5	475	2 Q6NZQ6	Q6NZQ6 homo sapien	
24	1578	90.5	480	2 Q6N094	Q6N094 homo sapien	
25	1578	90.5	481	2 Q6N097	Q6N097 homo sapien	
26	1578	90.5	482	2 Q7Z351	Q7Z351 homo sapien	
27	1577	90.5	544	2 Q6UJ95	Q6UJ95 homo sapien	
28	1575	90.4	466	2 Q6A096	Q6A096 homo sapien	
29	1571	90.1	475	2 Q6N095	Q6N095 homo sapien	
30	1561.5	89.9	521	2 QBNAY9	QBNAY9 homo sapien	
31	1558.5	89.4	518	2 Q6N030	Q6N030 homo sapien	

RESULT 1						
GC2_HUMAN						
ID	GC2_HUMAN	STANDARD	PRT	326 AA.		
AC	P01859;					
DT	21-JUL-1986 (Rel. 01, Created)					
DT	21-JUL-1986 (Rel. 01, Last sequence update)					
DT	05-JUL-2004 (Rel. 44, Last annotation update)					
DE	Ig gamma-2 chain C region.					
GN	Name:IGHG2;					
OS	Homo sapiens (Human)					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE OF 2-326 FROM N.A.					
RX	MEDLINE=81197621; PubMed=6801948;					
RA	Ellison J.W., Hood L.E.					
RT	"Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes";					
RT	chain genes and the linkage of the gamma 2 and gamma 4 subclass genes";					
RL	Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988 (1982).					
RN	[2]					
RP	SEQUENCE OF 88-1115 FROM N.A.					
RC	TISSUE=Fetal liver					
RX	MEDLINE=81001943; PubMed=6811139; DOI=10.1016/0092-8674(82)90183-0;					
RA	Nakaido T., Nakai S., Honjo T.;					
RT	"Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";					
RT	Cell 29:671-679 (1982).					
RN	[3]					
RP	SEQUENCE OF 99-1177 AND 310-326 FROM N.A.					
RC	TISSUE=Fetal liver					
RX	MEDLINE=84235932; PubMed=6329676;					
RA	Krawinkel U., Rabbits T.H.					
RT	"Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes";					
RT	Immunol. 125:1048-1054 (1980).					
RL	J. Immunol. 140:403-407 (1982).					
RN	[4]					
RP	SEQUENCE OF 1-325 (MYELOMA PROTEIN T1).					
RX	MEDLINE=81010783; PubMed=674012.					
RA	Wang A.-C., Tang E., Fudenberg H.H.					
RA	"The primary structure of a human IgG2 Heavy chain: genetic, evolutionary, and functional implications";					
RT	domains of a human IgG2 myeloma protein.";					
RT	Can. J. Biochem. 57:758-767 (1979).					
RN	[5]					
RP	SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).					
RX	MEDLINE=8001357; PubMed=113606;					
RA	Connell G.E., Parr D.M., Hofmann T.					
RA	"The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";					
RL	Can. J. Biochem. 57:758-767 (1979).					
RN	[6]					
RP	SEQUENCE OF 238-275 (ZIE).					
RX	MEDLINE=80114419; PubMed=118920; DOI=10.1016/0161-5890(79)90091-9;					

Hofmann T., Parr D.M.; "A note of the amino acid sequence of residues 381-391 of human immunoglobulin Gamma Chains"; Mol. Immunol. 16: 923-925(1979).
 [7]
 REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 Hofmann T., Parr D.M.; Submitted (MAY-1980) to the PIR data bank.
 [8]
 SEQUENCE OF 1-121 (DOT).
 MEDLINE=9255238; PubMed=737190;
 Stoppani M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.; "Characterization of the two unique human anti'-flavin monoclonal immunoglobulins"; Eur. J. Biochem. 228:886-893 (1995).
 [9]
 DISULFIDE BONDS;
 MEDLINE=72033500; PubMed=4940472;
 Milstein C., Frangione B.; "Structural studies of immunoglobulin G2"; Biochim. J. 121:217-225 (1971).
 [10]
 EMBL; J00230; AAB59393.1; -.
 PIR; A93906; GRHU.
 Genen, HGNC: 5526; IGHG2.
 HSSP; P01857; 1QX.
 GO; GO:0005624; C:membrane fraction; NAS.
 GO; GO:0003823; F:antigen binding; TAS.
 GO; GO:0006555; P:immune response; NAS.
 InterPro; IPR07110; Ig-like.
 InterPro; IPR03597; Ig_C1.
 Pfam; PF00047; Ig_3.
 SMART; SM00407; IgC1_2.
 PROSITE; PS00835; Ig_LIKE_3.
 PROSITE; PS00290; Ig_MHC_2.
 Direct protein sequencing; Immunoglobulin C region; Immunoglobulin domain.
 NON_TER 1 1
 DOMAIN 1 98 CH1.
 DOMAIN 1 99 110 Hinge.
 DOMAIN 111 219 CH2.
 DOMAIN 220 326 CH3.
 DISUFID 14 83 Interchain (with a light chain).
 DISUFID 27 83 Interchain (with a heavy chain).
 DISUFID 102 102 Interchain (with a heavy chain).
 DISUFID 103 103 Interchain (with a heavy chain).
 DISUFID 106 106 Interchain (with a heavy chain).
 DISUFID 109 109 At or near the complement-binding site.
 DISUFID 140 200 S->A (in myeloma proteins TIL and ZIE).
 DISUFID 246 304 /FTD>VAR 00388.
 SITE 156 156 Variant 60 60 CONFLICT 109 109 C->S (in Ref. 3).
 SEQUENCE 326 AA; 35884 MW; 8310878CC6878C9C CRC64;
 QUERY MATCH

Best Local Similarity	98.5%	Pred. No.	1.1e-116;
Matches	321;	Conservative	2;
Indels	3;	Gaps	0;
Qy	1 ASTKGPSVPLAPCSRSTESTAALGLVYKDYPEPEPVTVSNNSGALTSGVHTFPVLOSS	60	
Db	1 ASTKGPSVPLAPCSRSTESTAALGLVYKDYPEPEPVTVSNNSGALTSGVHTFPVLOSS	60	
Qy	61 GLYSISSLVTTVPSSNFGTQTYCNVDHKPSNTVKDVKVERKCCVECPGPAPPAAAPSVF	120	
Db	61 GLYSISSLVTTVPSSNFGTQTYCNVDHKPSNTVKDVKVERKCCVECPGPAPPAAAPSVF	120	
Qy	121 LFPPPKDKXIMISRTEPVTCVVYDVSHEDPEVQFNWYDGVVEHNAKTKPREEOFNSTFR	180	
Db	121 LFPPPKDKXIMISRTEPVTCVVYDVSHEDPEVQFNWYDGVVEHNAKTKPREEOFNSTFR	180	
Qy	181 VVSVLTVYHQDWLNGKEYKCKVSNKGFLAPIEKTISKTKGQPEPVQVYTLPPSPBEMTN	240	
Db	181 VVSVLTVYHQDWLNGKEYKCKVSNKGFLAPIEKTISKTKGQPEPVQVYTLPPSPBEMTN	240	
Qy	241 QVSLTCLVKGFPYDIAWEWSQOPENNYKTPPMILDSDGSFLYSLKLTVDKSRWQOGN	300	
Db	241 QVSLTCLVKGFPYDIAWEWSQOPENNYKTPPMILDSDGSFLYSLKLTVDKSRWQOGN	300	
Qy	301 VFSCSVXHEALHHHYTQKSLSSLSSK	326	
Db	301 VFSCSVXHEALHHHYTQKSLSSLSSK	326	
<hr/>			
RESULT	2		
Q6N093	PRELIMINARY;	PRT;	417 AA.
ID	Q6N093		
AC	Q6N093;		
DT	05-JUL-2004 (TREMBL); 27, Created		
DT	05-JUL-2004 (TREMBL); 27, Last sequence update		
DT	05-JUL-2004 (TREMBL); 27, Last annotation update		
DE	Hypothetical protein DKF2p686104196 (Fragment).		
GN	Name=DKF2p686104196;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX			
RN	NCBI_TaxID=9606;		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-Human esophagus tumor;		
RG	The German Human CDNA Consortium;		
RA	Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,		
RA	Fobo G., Han M., Wiemann S.,		
RL	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.		
EMBL	BX640633; CAE45777.1; -.		
DR	HSSP; P01861; 1ADQ		
DR	InterPro; IPR03598; Ig.		
DR	InterPro; IPR07110; Ig-like.		
DR	InterPro; IPR003597; Ig_C1.		
DR	InterPro; IPR00068; Ig_MHC.		
DR	InterPro; IPR003596; Ig_V.		
DR	Pfam; PF07654; Cl-set; Ig.		
DR	SMART; SM00408; Ig_2.		
DR	SMART; SM00407; Ig1; .		
DR	SMART; SM00406; IgV; 1.		
DR	PROSITE; PS00835; Ig_LIKE_3.		
DR	PROSITE; PS00090; Ig_MHC; UNKNOWN_2.		
KW	Hypothetical protein_NON_TER.		
FT	NON_TER 1 1		
SQ	SEQUENCE 417 AA; 46061 MW; C4518B844CFBB83C CRC54;		
Query Match	99.3%; Score 1731; DB 2;		
Best Local Similarity	98.5%; Pred. No. 1.6e-116;		
Matches	321;	Conservative	2;
Indels	3;	Gaps	0;
Qy	1 ASTKGPSVPLAPCSRSTESTAALGLVYKDYPEPEPVTVSNNSGALTSGVHTFPVLOSS	60	
Db	92 ASTKGPSVPLAPCSRSTESTAALGLVYKDYPEPEPVTVSNNSGALTSGVHTFPVLOSS	151	